AMENDMENTS TO THE SPECIFICATION

Please amend the section entitled "Cross-reference to Related Applications," beginning on page 1, line 8 and continuing through line 11 on page 1 as follows:

This application is a divisional application of U.S. Patent Application No. 10/066,130, filed January 31, 2002, now U.S. Patent No. 6,699,657, which claims the benefit of U.S. Provisional Application No. 60/265,437, filed January 31, 2001, the contents of which are herein incorporated by reference in their entirety.

Please amend the section beginning on page 10, line 25 and ending on page 11, line 23 as follows:

"Virally-compatible cells which have been transfected with the cDNA of the genomic sequence of an RDRP virus" refers to virally-compatible cells into which have been stably incorporated a functional genomic sequence of the virus under study. When the method is conducted in order to study and measure replication of the viral genome, it will be preferable to incorporate most or all of the native viral genomic sequence, in order to most effectively mimic and study native replication. When the method is conducted in order to identify inhibitors of viral replication, it is possible to incorporate into the cellular genome all of the genome, or alternatively only those selective portions of the viral genome which encode proteins to be studied, so long as the selected portion of the viral genome includes the sequence that encodes the RNA-dependent RNA polymerase, which is known as the NS5B portion of the HCV genome. Methods for stably transfecting all or selective portions of the viral genome into suitable cell lines are known by those skilled in the art. For example, such methods are reported in "Continuous Human Cell Lines Inducibly Expressing Hepatitus C Virus Structural and Nonstructural Proteins," Darius Marpour, Petra Kary, Charles M. Rice and Huber E. Blum (1998) Hepatology 28:192201. "Transfection of a Differentiated Human Hepatoma Cell Line (Huh7) with In Vitro-Transcribed Hepatitis C Virus (HCV) RNA and Establishment of a Long-Term Culture Persistently Infected with HCV," Young J. Yoo et al, J. of Virology, Vol 69, No.1, Jan 1995, p. 32-38. Genomic sequences for the flaviviruses are generally available in the scientific literature, for example, see ~~www.ncbi.nlm.nih.gov/genbank for~~ the Genbank library of sequences, which ~~that~~ includes viral and the *flavivirus* gene sequences.

Please amend the section entitled "Brief Description of the Drawings," beginning on page 8, line 12 and continuing through page 9, line 2, as follows:

Figure 1. Schematic for production of RDRP-dependent luciferase activity in the 293B4α cell line.

Figure 2. Cloning strategy for the construction of pMJ050.

Figure 3. Nucleotide sequence of pMJ050, presented from left to right in 5' to 3' orientation, Fig. 3A. showing the nucleotides comprising the SV40 promoter; and the HCV 3'UTR (in antisense orientation); Fig 3B showing the luciferase coding region (in antisense orientation); the HCV 5' UTR sequence (in antisense orientation); the hepatitis δ virus ribozyme sequence (in sense orientation); and Fig 3C. the plasmid backbone sequence.

Figure 4. Production of luciferase in 293FL#9 cells stably transfected with pMJ050.

Figure 5. Production of luciferase, HCV core, HCV serine protease, and HCV RDRP in the 293B4α cell line.

Figure 6. Production of luciferase sense and antisense RNA in the 293B4α cell line.

~~Figure 7. Schematic representation of the mechanism of the invention in a B4alpha human kidney cell which has been transfected with the genome of HCV, using luciferase as the reporter gene in a construct of the invention.~~